

Conference Abstract

Towards FAIR Principles in Biodiversity Research: Enabling computable taxonomic descriptions and ecological data with Phenoscript

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Received: 29 Aug 2023 | Published: 30 Aug 2023

Citation: Tarasov S, Montanaro G, Losacco F, Porto D (2023) Towards FAIR Principles in Biodiversity Research: Enabling computable taxonomic descriptions and ecological data with Phenoscript. Biodiversity Information Science and Standards 7: e111862. <https://doi.org/10.3897/biss.7.111862>

Abstract

Taxonomic descriptions hold immense phenotypic data, but their natural language (NL) format poses challenges for computer analysis. In this talk, we will present [Phenoscript](#), a user-friendly computer language enabling computer-readable species descriptions and automated phenotype comparisons, in accordance with [FAIR](#) (Findable, Accessible, Interoperable, Reusable) principles.

Phenoscript facilitates the creation of semantic species descriptions that represent a knowledge graph composed of terms from predefined biological ontologies. A Phenoscript description resembles a NL description, but follows a specific language grammar. We have developed the [Phenospy](#) package: a Python-based Phenoscript toolkit. Phenospy converts Phenoscript descriptions into both NL format, facilitating scientific publication, and the Web Ontology Language ([OWL](#)) format, enabling downstream analysis and computable phenotypic comparisons. OWL is a standard for sharing semantic data on the Web. While initially designed for phenotypes, Phenoscript can be extended to create semantic ecological data, encompassing environmental traits, functional traits, and species interactions. We will discuss the integration of species and ecological traits encoded in Phenoscript into downstream analysis, highlighting its potential for phenomic-level research in biology.

Keywords

semantic description, taxonomy, phenomics, ecology, ontologies, FAIR data

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Presented at

TDWG 2023

Funding program

This work received funding from the Academy of Finland (346294 and 339576 awarded to S.T.).

Conflicts of interest

The authors have declared that no competing interests exist.